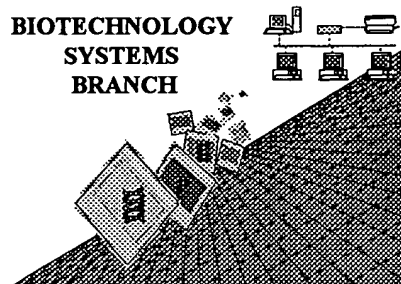


Devi

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

08/870,762

Art Unit / Team No. :

164/

Date Processed by STIC:

4/3/98

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/870,762DATE: 04/03/98
TIME: 14:40:10

INPUT SET: S24665.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: Duft, Bradford
6 Kolterman, Orville
7
8 (ii) TITLE OF THE INVENTION: METHODS FOR TREATING OBESITY
9
10 (iii) NUMBER OF SEQUENCES: 15
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: LYON & LYON
14 (B) STREET: 633 WEST FIFTH STREET, SUITE 4700
15 (C) CITY: LOS ANGELES
16 (D) STATE: CA
17 (E) COUNTRY: USA
18 (F) ZIP: 90071-2066
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Diskette
22 (B) COMPUTER: IBM Compatible
23 (C) OPERATING SYSTEM: DOS
24 (D) SOFTWARE: FastSEQ Version 2.0
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: 08/870,762
28 (B) FILING DATE: 06-JUN-1997
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER:
33 (B) FILING DATE:
34
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: DUFT, BRADFORD J
38 (B) REGISTRATION NUMBER: 32,219
39 (C) REFERENCE/DOCKET NUMBER: 226/104
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: 619-552-8400
43 (B) TELEFAX: 619-552-0159
44 (C) TELEX:
45
46

Does Not Comply
Corrected Diskette Needed
P.4

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/870,762DATE: 04/03/98
TIME: 14:40:10

INPUT SET: S24665.raw

47 (2) INFORMATION FOR SEQ ID NO:1:

48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 37 amino acids

51 (B) TYPE: amino acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

54

55 (ii) MOLECULE TYPE: peptide

56

57 (ix) FEATURE:

58 (B) LOCATION: 2,7

59 (D) OTHER INFORMATION: disulfide bridge between
60 the Cys residues

61 (B) LOCATION: 37

62 (D) OTHER INFORMATION: amidated Tyr

63

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

65

66

67 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

68 1 5 10 15

69 Leu Val His Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr

70 20 25 30

71 Asn Val Gly Ser Asn Thr Tyr

72 35

73

74 (2) INFORMATION FOR SEQ ID NO:2:

75

76 (i) SEQUENCE CHARACTERISTICS:

77 (A) LENGTH: 37 amino acids

78 (B) TYPE: amino acid

79 (C) STRANDEDNESS: single

80 (D) TOPOLOGY: linear

81

82 (ii) MOLECULE TYPE: peptide

83

84 (ix) FEATURE:

85 (B) LOCATION: 2,7

86 (D) OTHER INFORMATION: disulfide bridge between
87 the Cys residues

88 (B) LOCATION: 37

89 (D) OTHER INFORMATION: amidated Tyr

90

91

92 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

93

94 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

95 1 5 10 15

96 Leu Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Pro Thr

97 20 25 30

98 Asn Val Gly Ser Asn Thr Tyr

99 35

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/870,762DATE: 04/03/98
TIME: 14:40:11

INPUT SET: S24665.raw

100
101
102
103 (2) INFORMATION FOR SEQ ID NO:3:
104
105 (i) SEQUENCE CHARACTERISTICS:
106 (A) LENGTH: 37 amino acids
107 (B) TYPE: amino acid
108 (C) STRANDEDNESS: single
109 (D) TOPOLOGY: linear
110
111 (ii) MOLECULE TYPE: Peptide
112
113 (ix) FEATURE:
114 (B) LOCATION: 2,7
115 (D) OTHER INFORMATION: disulfide bridge between
116 the Cys residues
117 (B) LOCATION: 37
118 (D) OTHER INFORMATION: amidated Tyr
119
120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
121
122 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
123 1 5 10 15
124 Leu Val Arg Ser Ser Asn Asn Phe Gly Pro Ile Leu Pro Ser Thr
125 20 25 30
126 Asn Val Gly Ser Asn Thr Tyr
127 35
128
129 (2) INFORMATION FOR SEQ ID NO:4:
130
131 (i) SEQUENCE CHARACTERISTICS:
132 (A) LENGTH: 37 amino acids
133 (B) TYPE: amino acid
134 (C) STRANDEDNESS: single
135 (D) TOPOLOGY: linear
136
137 (ii) MOLECULE TYPE: Peptide
138
139 (ix) FEATURE:
140 (B) LOCATION: 2,7
141 (D) OTHER INFORMATION: disulfide bridge between
142 the Cys residues
143 (B) LOCATION: 37
144 (D) OTHER INFORMATION: amidated Tyr
145
146 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
147
148 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe
149 1 5 10 15
150 Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Pro Ser Thr
151 20 25 30
152 Asn Val Gly Ser Asn Thr Tyr

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/870,762DATE: 04/03/98
TIME: 14:40:12

INPUT SET: S24665.raw

153

35

154

155

(2) INFORMATION FOR SEQ ID NO:5:

156

157

(i) SEQUENCE CHARACTERISTICS:

158

(A) LENGTH: 37 amino acids

159

(B) TYPE: amino acid

160

(C) STRANDEDNESS: single

161

(D) TOPOLOGY: linear

162

163

(ii) MOLECULE TYPE: peptide

164

165

(ix) FEATURE:

166

(B) LOCATION: 2,7

167

(D) OTHER INFORMATION: disulfide bridge between
the Cys residues

168

169

(B) LOCATION: 37

170

(D) OTHER INFORMATION: amidated Tyr

171

172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

173

174

Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

175

1 5 10 15

176

Leu Val His Ser Ser Asn Asn Phe Gly Pro Val Leu Pro Pro Thr

177

20 25 30

178

Asn Val Gly Ser Asn Thr Tyr

179

35

180

181

182

(2) INFORMATION FOR SEQ ID NO:6:

183

184

(i) SEQUENCE CHARACTERISTICS:

185

(A) LENGTH: 37 amino acids

186

(B) TYPE: amino acid

187

(C) STRANDEDNESS: single

188

(D) TOPOLOGY: linear

189

190

(ii) MOLECULE TYPE: peptide

191

192

(ix) FEATURE:

193

(B) LOCATION: 2,7

194

(D) OTHER INFORMATION: disulfide bridge between
the Cys residues

195

196

(B) LOCATION: 37

197

(D) OTHER INFORMATION: amidated Tyr

198

199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

200

201

Lys Asp Asn Thr Ala Thr Lys Ala Thr Gln Arg Leu Ala Asn Phe

202

1 5 10 15

203

Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr

204

20 25 30

205

Asn Val Gly Ser Asn Thr Tyr

"Cys" is not shown in location 2 and 7

Please edit
any subsequent
sequences (showing
this error)

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/870,762DATE: 04/03/98
TIME: 14:40:14

INPUT SET: S24665.raw

206

35

207

208

209

(2) INFORMATION FOR SEQ ID NO:7:

210

211

(i) SEQUENCE CHARACTERISTICS:

212

(A) LENGTH: 37 amino acids

213

(B) TYPE: amino acid

214

(C) STRANDEDNESS: single

215

(D) TOPOLOGY: linear

216

217

(ii) MOLECULE TYPE: peptide

218

219

(ix) FEATURE:

220

(B) LOCATION: 2,7

221

(D) OTHER INFORMATION: disulfide bridge between
the Cys residues

222

223

(B) LOCATION: 37

224

(D) OTHER INFORMATION: amidated Tyr

225

226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

227

228 Lys Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

229

1

5

10

15

230

Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr

231

20

25

30

232

Asn Val Gly Ser Asn Thr Tyr

233

35

234

235

(2) INFORMATION FOR SEQ ID NO:8:

236

237

(i) SEQUENCE CHARACTERISTICS:

238

(A) LENGTH: 37 amino acids

239

(B) TYPE: amino acid

240

(C) STRANDEDNESS: single

241

(D) TOPOLOGY: linear

242

243

(ii) MOLECULE TYPE: peptide

244

245

(ix) FEATURE:

246

(B) LOCATION: 2,7

247

(D) OTHER INFORMATION: disulfide bridge between
the Cys residues

248

249

(B) LOCATION: 37

250

(D) OTHER INFORMATION: amidated Tyr

251

252

253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

254

255

Ala Cys Asn Thr Ala Thr Cys Ala Thr Gln Arg Leu Ala Asn Phe

256

1

5

10

15

257

Leu Val His Ser Ser Asn Asn Phe Gly Ala Ile Leu Ser Ser Thr

258

20

25

30

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/870,762

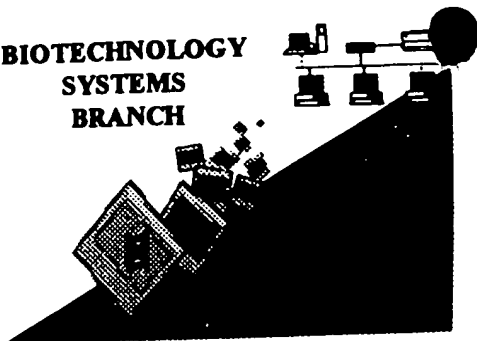
DATE: 04/03/98
TIME: 14:40:15

INPUT SET: S24665.raw

Line

Error

Original Text



Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF)
Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CFR 1.821 through 1.825). Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

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The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>
The software is in current directory: `pub/checker/`
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
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For Further Information, Contact: Arti Shah at 703-308-4212